Thailand over the first two waves of the epidemic by tracking variation in the effective reproduction number, *R*t, which measures the average number of secondary cases per case.

Methods: Laboratory-confirmed cases (cases positive for influenza A/H1N1pdm 2009 by real-time PCR) were used as input data for the estimation procedure. Data points corresponded to dates of symptom onset of influenza A/H1N1pdm in Thailand from 3 May 2009 to 26 December 2010 in four geographic regions (central, north, north-east, and south). We analyzed these data using a previously described approach of epidemic reconstruction to derive estimates of how the effective reproduction number, *R*t, varied with region and over time. Confidence intervals were calculated using a bootstrap procedure.

Results: We found that the estimated *R*t values for the first wave peaked at 1.5 (with 95% CI, 1.4-1.7) in the central region and 1.6 (95% CI, 1.4-1.9) in the north, whilst the corresponding values in the north-east and the south were close to 1.3. By the time that the *R*t estimate in the central region was below one, the value of *R*t in the rest of Thailand had started to increase above one. The value of *R*t in the first wave was estimated to be above one continuously for 30 days in all regions. For the second wave, the *R*t estimates were only marginally above one within the first three months in all regions except the south.

Conclusion: The estimate values of *R*t for the first and the second waves of the influenza A H1N1pdm epidemic in Thailand varied by region, with higher estimates obtained from the central and northern regions in the first wave. Accounting for regional variation in transmission potential is important for helping to predict the course of future pandemics and for analysing potential control measures (i.e. regionally-targeted control policies).

http://dx.doi.org/10.1016/j.ijid.2012.05.436

Type: Poster Presentation

Final Abstract Number: 53.037
Session: Epidemiology & Public Health
Date: Saturday, June 16, 2012
Time: 12:45-14:15
Room: Poster & Exhibition Area

Epidemiological situation of malaria infections in Nikshahr: A city in the endemic area of Sistan and Balouchestan province, Southeastern Iran

B. Sharifi-Mood[1], M. Metanat[2,*], N. Sepehrirad[2], N. Arbabi[3], M. Sakeni[4], R. Gholizadeh Doran Mahaleh[5]

[1] *Research Center for Infectious Diseases and Tropical Medicine, Boo-Ali Hospital,Zahedan University of Medical Sciences, Zahedan, Iran, Islamic Republic of*
[2] *Research Center for Infectious Diseases and Tropical Medicine, Boo-Ali Hospital,Zahedan University of Medical Sciences, Zahedan, Siatan&Baloochestan, Iran, Islamic Republic of*
[3] *Research center for infectious diseases and tropical medicine, Zahedan, Iran, Islamic Republic of*
[4] *Department of Health, Zahedan University of Medical Siences, Zahedan, Iran, Islamic Republic of*
[5] *Islamic Azad University, Zahedan, Iran, Islamic Republic of*

Background: Malaria, one of the most important health problem in tropical and subtropical regions is an endemic disease appeared in the Southeastern province of Iran.This descriptive study conducted to show the epidemiological feature of Malaria grams during the March 2006-March2010.

Methods: This study is a descriptive epidemiological study of Malaria. Information extracted from the monthly report forms collected by the department of health, at Zahedan university of medical sciences. Peripheral blood smears were taken from all patients who had fever. Slides were prepared in both thin film at one end and thick film at the other side and were stained with Giemsa and examined under microscope by 100X magnification. Data from completed forms of epidemiology for all positive cases were analyzed in this study.

Results: A total of 30783 reported Malaria infections from the year 2006 to 2010 were investigated, 7035(22.8%) cases were isolated from the patients in Nikshahr city. 4183(59.4%) of these patients were male and 2852(40.5%) were female. 74 cases of women were pregnant. The highest infection rate observed in the patients above 15 years old (4236 cases, 60.2%) . Malaria was seen in patients between 5-14 years and less than 4 years 2227cases, 31.6%), (572, 8.1%), respectively. According to these data, 6965(99%) of isolated species were *Plasmodium vivax*, 50(0.7%) *Plasmodium falciparum* and 20(0.2%) were found to be mixed species. Ninety-six percent(7666 cases) of patients were Iranian, 221 cases (3%) Afghan immigrants and 47(0.6%) Pakistani immigrants.

Conclusion: This study showed that *Plasmodium vivax* is the most infection of Malaria in this area and the infectrion has declined from 2937 cases in the year 2006 to the 138 cases in 2010. No case of *Plasmodium falciparum* detected in 2010. More public knowledge, health centers control, use of mosquito-net in endemic region and immigrants control were the probable reasons of Malaria decline during the past recent years.

http://dx.doi.org/10.1016/j.ijid.2012.05.437

Type: Poster Presentation

Final Abstract Number: 53.038
Session: Epidemiology & Public Health
Date: Saturday, June 16, 2012
Time: 12:45-14:15
Room: Poster & Exhibition Area

Why are so many infants getting measles in China?

J. Montgomery[1,*], X. Wang[2], B. Carlson[1], Y. Zhang[2], B. Gillespie[1], A. Wagner[1], M. Boulton[1]

[1] *University of Michigan, Ann Arbor, MI, USA*
[2] *Tianjin Centers for Disease Control and Prevention, Tianjin, China*

Background: According to the World Health Organization (WHO), measles is the leading global cause of vaccine-preventable mortality and the fifth leading cause of all childhood mortality. Furthermore, WHO estimates 20 million individuals are infected with measles every year.

China is targeted for measles elimination by 2012 as part of the WHO's Western Pacific Region elimination plan. From 2002 to 2008, China experienced an increase in measles incidence from 4.8 to 9.9 per 100,000 persons. In 2010 in Tianjin, China, a municipality of approximately 10.4 million persons, nearly 600 cases of measles were reported in children under age 1 year (a rate of approximately 450 per 100,000 persons in this age group). Despite control efforts, sustained levels of endemic transmission present challenges to accomplishing the goal of elimination.

Methods: A research collaborative between the University of Michigan and the Tianjin Centers for Disease Control and Preven-

tion is currently conducting a population-based cross-sectional study throughout the province of Tianjin to describe risk factors for the acquisition of measles and to estimate the sero-prevalence of measles antibodies. The study consists of a brief interview and collection of a dried bloodspot specimen in consenting people <50 years-old. Included in this study is a subset of mother/infant pairs.

Results: Preliminary results from 16 mother/infant pairs indicate that while most (100%) mothers have adequate measles antibody levels, many of their infants aged 3-8 months do not have adequate protection (85%). Immunization for measles is recommended at age 8 months in Tianjin, funding for which is provided by the government. Antibody levels in children 8 months and older are correspondingly adequate (88%). The study is progressing rapidly, and more up to date information will be presented.

Conclusion: While the waning of maternal antibodies in infants has been a well-documented concern, we found evidence that this may be occurring at a younger age than previously documented. Although our results are preliminary, this issue could have major ramifications for vaccination and control programs throughout China and perhaps globally.

http://dx.doi.org/10.1016/j.ijid.2012.05.438

Type: Poster Presentation

Final Abstract Number: 53.039
Session: Epidemiology & Public Health
Date: Saturday, June 16, 2012
Time: 12:45-14:15
Room: Poster & Exhibition Area

Comparison of influenza A(H1N1)pdm09 mortality with seasonal influenza mortality in Australia

D. Muscatello[1,*], R. MacIntyre[2], D. Dwyer[3], A. Newall[4]

[1] *University of New South Wales, Kensington, NSW, Australia*
[2] *University of New South Wales, Kensington, Australia*
[3] *University of Sydney, Camperdown, Australia*
[4] *University of New South Wales, Sydney, Australia*

Background: In 2009, large numbers of pandemic influenza deaths were recorded. However, assessment of influenza-related mortality using laboratory confirmation suffers from under-ascertainment.

To overcome this difficulty, statistical methods are often applied to population mortality time series to estimate the excess deaths that occur during influenza epidemics. A common feature of these methods is to estimate background, non-influenza, mortality using a regression model with harmonic parameters for seasonality, based on the method introduced by Serfling in the 1960s.

A limitation of the harmonic model is that it requires the seasonal background to have the same shape and magnitude each year. In Australia, this requirement provides a poor fit to the observed mortality time series.

Methods: We used a generalized additive model with a smoothing spline function of time to provide a more flexible fit to the background weekly mortality. Time series of Australian death rates, 2003 to 2009, from respiratory, respiratory and circulatory causes, and all-causes were the outcome variables examined. Incorporating laboratory virology time series into the model allowed us to estimate the contribution of influenza A (H1N1)pdm09, seasonal influenza A and B, and respiratory syncytial virus (RSV).

Results: For persons of all ages in 2009 in Australia, preliminary model estimates indicated a respiratory mortality rate associated with influenza A(H1N1)pdm09 of 0.9 (95% confidence interval – CI 0.4-1.9) per 100,000, or 199 (95% CI 87-311) deaths. For all-cause mortality, the estimates were 2.3 (95% CI 0.2-4.4) per 100,000, or 501 (95% CI 51-951) deaths.

In comparison, public health surveillance records in Australia in 2009 indicated there were 191 deaths (0.9 per 100,000) in which a laboratory-confirmed A(H1N1)pdm09 infection was recorded.

In the years studied, the greatest model-estimated seasonal influenza A all-cause death rate occurred in 2007 – rate 11.6 (95% CI 9.7-13.5) per 100,000, count 2412 (95% CI 2019-2805).

Conclusion: Seasonal influenza-related deaths in Australia in 2007 may have occurred at a rate 5 times greater than that of pandemic influenza in 2009. This observation may relate at least partly to the differing age distribution of susceptibility to the different influenza strains.

http://dx.doi.org/10.1016/j.ijid.2012.05.439

Type: Poster Presentation

Final Abstract Number: 53.040
Session: Epidemiology & Public Health
Date: Saturday, June 16, 2012
Time: 12:45-14:15
Room: Poster & Exhibition Area

Is there any association between brucellosis and the development of atherosclerotic heart disease?

A.R. Bizri, U. Musharrafieh*, S. Alam, A. Choukair, H. Tamim

American University of Beirut - Medical Center, Beirut, Lebanon

Background: Previous studies have suggested an infectious link to atherosclerosis. It was hypothesized that there exists a role for Brucella in triggering cardiovascular events by causing a chronic inflammatory state. In this study Brucella was explored as a possible candidate pathogen, pathogenetically related to the development of atherosclerosis.

Methods: Patients referred for coronary angiography were studied. Subjects were categorized into two groups; those with greater than 75% stenosis in at least one coronary artery and those with less than 75% stenosis. Risk factors for coronary artery disease were recorded and blood was obtained for brucella titers (direct and indirect) and C-reactive protein levels

Results: A total of 424 patients were included in the study (72.2% males and 27.8% females). Among patients with positive Brucella titers (direct or indirect), 70.6% had CAD. Among patients with negative Brucella titers 74.9% had CAD. The difference between these two groups did not reach statistical significance ($P = 0.514$). The variables found to be predictors of CAD were gender ($P = 0.003$), history of diabetes ($P = 0.005$), hyperlipidemia ($P < 0.001$) and statin intake ($P < 0.001$). Patients with highly elevated CRP (>6), 63.2% had at least one vessel disease greater than 75% whereas patients with lower CRP levels (<3 or CRP 3-6), 44.3% and 45.8% had vessel disease greater than 75%, respectively ($P = 0.001$).

Conclusion: Conclusions:The findings do not suggest an association between chronic brucellosis, tested by direct and indirect antibody tests, and the development of CAD, but a correlation between brucella antibody positivity and elevated CRP was found to be significant.

http://dx.doi.org/10.1016/j.ijid.2012.05.440